

CRF Errors Edited by the STIC Systems Branch

Serial Number: 10/506, 624

CRF Edit Date: 9/13/04
Edited by: KL

 Realigned nucleic acid/amino acid numbers/text in cases where the sequence text "wrapped" to the next line

 Corrected the SEQ ID NO. Sequence numbers edited were:

ENTERED

 Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited:

☒ Deleted: ☒ invalid beginning/end-of-file text ; page numbers

 Inserted mandatory headings/numeric identifiers, specifically:

 Moved responses to same line as heading/numeric identifier, specifically:

 Other:



PCT

RAW SEQUENCE LISTING

DATE: 09/13/2004

PATENT APPLICATION: US/10/506,624

TIME: 16:13:21

Input Set : A:\pto.kd.txt

Output Set: N:\CRF4\09132004\J506624.raw

3 <110> APPLICANT: Yamanouchi Pharmaceutical Co., Ltd.
 5 <120> TITLE OF INVENTION: Novel potassium-dependent sodium/calcium exchanger
 7 <130> FILE REFERENCE: Y0335PCT-693
 C--> 9 <140> CURRENT APPLICATION NUMBER: US/10/506,624
 C--> 9 <141> CURRENT FILING DATE: 2004-09-03
 9 <150> PRIOR APPLICATION NUMBER: JP 2002-225114
 10 <151> PRIOR FILING DATE: 2002-08-01
 12 <150> PRIOR APPLICATION NUMBER: JP 2003-182989
 13 <151> PRIOR FILING DATE: 2003-06-26
 15 <160> NUMBER OF SEQ ID NOS: 8
 17 <170> SOFTWARE: PatentIn version 3.1
 19 <210> SEQ ID NO: 1
 20 <211> LENGTH: 1902
 21 <212> TYPE: DNA
 22 <213> ORGANISM: Homo sapiens
 24 <220> FEATURE:
 25 <221> NAME/KEY: CDS
 26 <222> LOCATION: (14)..(1882)
 27 <223> OTHER INFORMATION:
 29 <220> FEATURE:
 30 <223> OTHER INFORMATION: Inventor: Nozawa, Katsura; Mochizuki, Shinobu
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 34 Met Ala Leu Arg Gly Thr Leu Arg Pro Leu Lys Val
 35 1 5 10
 37 cgc agg agg cga gag atg ctg ccg cag caa gtc ggc ttc gtg tgc gcg 97
 38 Arg Arg Arg Arg Glu Met Leu Pro Gln Gln Val Gly Phe Val Cys Ala
 39 15 20 25
 41 gtg ctg gcc ctg gtg tgc tgt gcg tcc ggc ctc ttc ggc agc ttg ggg 145
 42 Val Leu Ala Leu Val Cys Cys Ala Ser Gly Leu Phe Gly Ser Leu Gly
 43 30 35 40
 49 cac aaa aca gct tct gct agc aaa cgt gtc ctg cca gac aca tgg aga 193
 50 His Lys Thr Ala Ser Ala Ser Lys Arg Val Leu Pro Asp Thr Trp Arg
 51 45 50 55 60
 53 aat aga aag ttg atg gcc cca gtg aat ggg aca cag aca gcc aag aac 241
 54 Asn Arg Lys Leu Met Ala Pro Val Asn Gly Thr Gln Thr Ala Lys Asn
 55 65 70 75
 57 tgc aca gat cct gcg att cac gag ttc ccc aca gat ctg ttc tcc aat 289
 58 Cys Thr Asp Pro Ala Ile His Glu Phe Pro Thr Asp Leu Phe Ser Asn
 59 80 85 90
 61 aag gag cga cag cac gga gcc gtc ctg ctg cac atc ctt ggt gct ctg 337
 62 Lys Glu Arg Gln His Gly Ala Val Leu Leu His Ile Leu Gly Ala Leu
 63 95 100 105

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Output Set: N:\CRF4\09132004\J506624.raw

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67	110 115 120	
69	tct cta gag aag atc tgt gag aga ctc cat ctg agc gaa gat gtg gct	433
70	Ser Leu Glu Lys Ile Cys Glu Arg Leu His Leu Ser Glu Asp Val Ala	
71	125 130 135 140	
73	gga gcc acc ttc atg gct gca gga agc tca acg cca gag ctg ttt gcg	481
74	Gly Ala Thr Phe Met Ala Ala Gly Ser Ser Thr Pro Glu Leu Phe Ala	
75	145 150 155	
77	tct gtt att ggg gtg ttc atc acc cac ggg gac gtc ggg gtg ggc acc	529
78	Ser Val Ile Gly Val Phe Ile Thr His Gly Asp Val Gly Val Gly Thr	
79	160 165 170	
81	atc gtg ggc tct gct gtg ttc aac atc ctg tgc ata att gga gtg tgc	577
82	Ile Val Gly Ser Ala Val Phe Asn Ile Leu Cys Ile Ile Gly Val Cys	
83	175 180 185	
85	gga ctg ttt gct ggc cag gtg gtc cgt ctg acg tgg tgg gcc gtg tgc	625
86	Gly Leu Phe Ala Gly Gln Val Val Arg Leu Thr Trp Trp Ala Val Cys	
87	190 195 200	
89	cga gac tcc gtg tac tac acc atc tct gtc atc gtg ctc atc gtg ttc	673
90	Arg Asp Ser Val Tyr Tyr Thr Ile Ser Val Ile Val Leu Ile Val Phe	
91	205 210 215 220	
97	ata tat gat gaa caa att gtg tgg tgg gaa ggc ctg gtg ctc atc atc	721
98	Ile Tyr Asp Glu Gln Ile Val Trp Trp Glu Gly Leu Val Leu Ile Ile	
99	225 230 235	
101	ttg tat gtg ttt tat att ctg atc atg aag tac aat gtg aag atg caa	769
102	Leu Tyr Val Phe Tyr Ile Leu Ile Met Lys Tyr Asn Val Lys Met Gln	
103	240 245 250	
105	gcc ttt ttc aca gtc aaa caa aag agc att gca aac ggt aac ccg gtc	817
106	Ala Phe Phe Thr Val Lys Gln Lys Ser Ile Ala Asn Gly Asn Pro Val	
107	255 260 265	
109	aac agt gag ctg gag gct ggt aat gat ttc tat gac ggt agc tat gat	865
110	Asn Ser Glu Leu Glu Ala Gly Asn Asp Phe Tyr Asp Gly Ser Tyr Asp	
111	270 275 280	
113	gac cct tcc gtg cca ttg ctg ggg caa gtg aag gag aag cca cag tat	913
114	Asp Pro Ser Val Pro Leu Leu Gly Gln Val Lys Glu Lys Pro Gln Tyr	
115	285 290 295 300	
117	ggc aag aac ccc gtg gtg atg gtg gac gag att atg agc tcc agc cct	961
118	Gly Lys Asn Pro Val Val Met Val Asp Glu Ile Met Ser Ser Ser Pro	
119	305 310 315	
121	ccc aag ttc acc ttc cct gaa gca ggc tta cga atc atg atc acc aat	1009
122	Pro Lys Phe Thr Phe Pro Glu Ala Gly Leu Arg Ile Met Ile Thr Asn	
123	320 325 330	
125	aag ttt gga ccc agg acc cga cta cgg atg gcc agc agg atc atc att	1057
126	Lys Phe Gly Pro Arg Thr Arg Leu Arg Met Ala Ser Arg Ile Ile Ile	
127	335 340 345	
129	aat gag cgg cag aga ctg atc aac tcg gcc aat ggt gtg agc agt aag	1105
130	Asn Glu Arg Gln Arg Leu Ile Asn Ser Ala Asn Gly Val Ser Ser Lys	
131	350 355 360	
133	ccg ctt caa aac ggg agg cac gag aac att gag aac ggg aat gtt cct	1153

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Input Set : A:\pto.kd.txt

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134	Pro	Leu	Gln	Asn	Gly	Arg	His	Glu	Asn	Ile	Glu	Asn	Gly	Asn	Val	Pro	
135	365					370					375					380	
137	gtg	gaa	aac	ccc	gaa	gac	cct	cag	cag	aat	cag	gag	cag	cag	ccg	ccg	1201
138	Val	Glu	Asn	Pro	Glu	Asp	Pro	Gln	Gln	Asn	Gln	Glu	Gln	Gln	Pro	Pro	
139					385					390						395	
145	cca	cag	cca	cca	ccg	cca	gag	cca	gag	ccg	gtg	gag	gct	gac	ttc	ctg	1249
146	Pro	Gln	Pro	Pro	Pro	Pro	Glu	Pro	Glu	Pro	Val	Glu	Ala	Asp	Phe	Leu	
147					400					405						410	
149	tcc	ccc	ttc	tcc	gtg	ccg	gag	gcc	aga	ggg	gac	aag	gtc	aag	tgg	gtg	1297
150	Ser	Pro	Phe	Ser	Val	Pro	Glu	Ala	Arg	Gly	Asp	Lys	Val	Lys	Trp	Val	
151			415						420					425			
153	ttc	acc	tgg	ccc	ctc	atc	ttc	ctc	ctg	tgc	gtc	acc	att	ccc	aac	tgc	1345
154	Phe	Thr	Trp	Pro	Leu	Ile	Phe	Leu	Leu	Cys	Val	Thr	Ile	Pro	Asn	Cys	
155		430					435						440				
157	agc	aag	ccc	cgc	tgg	gag	aag	ttc	ttc	atg	gtc	acc	ttc	atc	acc	gcc	1393
158	Ser	Lys	Pro	Arg	Trp	Glu	Lys	Phe	Phe	Met	Val	Thr	Phe	Ile	Thr	Ala	
159	445					450					455					460	
161	acg	ctg	tgg	atc	gct	gtg	ttc	tcc	tac	atc	atg	gtg	tgg	ctg	gtg	act	1441
162	Thr	Leu	Trp	Ile	Ala	Val	Phe	Ser	Tyr	Ile	Met	Val	Trp	Leu	Val	Thr	
163					465						470					475	
165	att	atc	gga	tac	aca	ctt	ggg	atc	ccg	gat	gtc	atc	atg	ggc	att	act	1489
166	Ile	Ile	Gly	Tyr	Thr	Leu	Gly	Ile	Pro	Asp	Val	Ile	Met	Gly	Ile	Thr	
167				480						485						490	
169	ttc	ctg	gca	gca	ggg	aca	agt	gtt	cca	gac	tgc	atg	gcc	agc	cta	att	1537
170	Phe	Leu	Ala	Ala	Gly	Thr	Ser	Val	Pro	Asp	Cys	Met	Ala	Ser	Leu	Ile	
171			495						500					505			
173	gtg	gcg	aga	caa	ggc	ctt	ggg	gac	atg	gca	gtc	tcc	aac	acc	ata	gga	1585
174	Val	Ala	Arg	Gln	Gly	Leu	Gly	Asp	Met	Ala	Val	Ser	Asn	Thr	Ile	Gly	
175		510					515						520				
177	agc	aac	gtg	ttt	gac	atc	ctg	gta	gga	ctt	ggt	gta	ccg	tgg	ggc	ctg	1633
178	Ser	Asn	Val	Phe	Asp	Ile	Leu	Val	Gly	Leu	Gly	Val	Pro	Trp	Gly	Leu	
179	525					530					535					540	
181	cag	acc	atg	gtt	gtt	aat	tat	gga	tca	aca	gtg	aag	atc	aac	agc	cgg	1681
182	Gln	Thr	Met	Val	Val	Asn	Tyr	Gly	Ser	Thr	Val	Lys	Ile	Asn	Ser	Arg	
183					545						550					555	
185	ggg	ctg	gtc	tat	tcc	gtg	gtc	ctg	ttg	ctg	ggc	tct	gtc	gct	ctc	acc	1729
186	Gly	Leu	Val	Tyr	Ser	Val	Val	Leu	Leu	Leu	Gly	Ser	Val	Ala	Leu	Thr	
187				560						565						570	
193	gtc	ctc	ggc	atc	cac	cta	aac	aag	tgg	cga	ctg	gac	cgg	aag	ctg	ggt	1777
194	Val	Leu	Gly	Ile	His	Leu	Asn	Lys	Trp	Arg	Leu	Asp	Arg	Lys	Leu	Gly	
195			575					580						585			
197	gtc	tac	gtg	ctg	gtt	ctc	tac	gcc	atc	ttc	ttg	tgc	ttc	tcc	ata	atg	1825
198	Val	Tyr	Val	Leu	Val	Leu	Tyr	Ala	Ile	Phe	Leu	Cys	Phe	Ser	Ile	Met	
199		590					595						600				
201	ata	gag	ttt	aac	gtc	ttt	acc	ttc	gtc	aac	ttg	ccg	atg	tgc	cgg	gaa	1873
202	Ile	Glu	Phe	Asn	Val	Phe	Thr	Phe	Val	Asn	Leu	Pro	Met	Cys	Arg	Glu	
203	605					610					615					620	
205	gac	gat	tag	cgctgagtcg	cggtacctgg												1902
206	Asp	Asp															

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DATE: 09/13/2004

PATENT APPLICATION: US/10/506,624

TIME: 16:13:21

Input Set : A:\pto.kd.txt

Output Set: N:\CRF4\09132004\J506624.raw

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210 <210> SEQ ID NO: 2
211 <211> LENGTH: 622
212 <212> TYPE: PRT
213 <213> ORGANISM: Homo sapiens
215 <400> SEQUENCE: 2
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218 1 5 10 15
221 Glu Met Leu Pro Gln Gln Val Gly Phe Val Cys Ala Val Leu Ala Leu
222 20 25 30
225 Val Cys Cys Ala Ser Gly Leu Phe Gly Ser Leu Gly His Lys Thr Ala
226 35 40 45
229 Ser Ala Ser Lys Arg Val Leu Pro Asp Thr Trp Arg Asn Arg Lys Leu
230 50 55 60
233 Met Ala Pro Val Asn Gly Thr Gln Thr Ala Lys Asn Cys Thr Asp Pro
234 65 70 75 80
241 Ala Ile His Glu Phe Pro Thr Asp Leu Phe Ser Asn Lys Glu Arg Gln
242 85 90 95
245 His Gly Ala Val Leu Leu His Ile Leu Gly Ala Leu Tyr Met Phe Tyr
246 100 105 110
249 Ala Leu Ala Ile Val Cys Asp Asp Phe Phe Val Pro Ser Leu Glu Lys
250 115 120 125
253 Ile Cys Glu Arg Leu His Leu Ser Glu Asp Val Ala Gly Ala Thr Phe
254 130 135 140
257 Met Ala Ala Gly Ser Ser Thr Pro Glu Leu Phe Ala Ser Val Ile Gly
258 145 150 155 160
261 Val Phe Ile Thr His Gly Asp Val Gly Val Gly Thr Ile Val Gly Ser
262 165 170 175
265 Ala Val Phe Asn Ile Leu Cys Ile Ile Gly Val Cys Gly Leu Phe Ala
266 180 185 190
269 Gly Gln Val Val Arg Leu Thr Trp Trp Ala Val Cys Arg Asp Ser Val
270 195 200 205
273 Tyr Tyr Thr Ile Ser Val Ile Val Leu Ile Val Phe Ile Tyr Asp Glu
274 210 215 220
277 Gln Ile Val Trp Trp Glu Gly Leu Val Leu Ile Ile Leu Tyr Val Phe
278 225 230 235 240
281 Tyr Ile Leu Ile Met Lys Tyr Asn Val Lys Met Gln Ala Phe Phe Thr
282 245 250 255
289 Val Lys Gln Lys Ser Ile Ala Asn Gly Asn Pro Val Asn Ser Glu Leu
290 260 265 270
293 Glu Ala Gly Asn Asp Phe Tyr Asp Gly Ser Tyr Asp Asp Pro Ser Val
294 275 280 285
297 Pro Leu Leu Gly Gln Val Lys Glu Lys Pro Gln Tyr Gly Lys Asn Pro
298 290 295 300
301 Val Val Met Val Asp Glu Ile Met Ser Ser Ser Pro Pro Lys Phe Thr
302 305 310 315 320
305 Phe Pro Glu Ala Gly Leu Arg Ile Met Ile Thr Asn Lys Phe Gly Pro
306 325 330 335
309 Arg Thr Arg Leu Arg Met Ala Ser Arg Ile Ile Ile Asn Glu Arg Gln
310 340 345 350

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RAW SEQUENCE LISTING

DATE: 09/13/2004

PATENT APPLICATION: US/10/506,624

TIME: 16:13:21

Input Set : A:\pto.kd.txt

Output Set: N:\CRF4\09132004\J506624.raw

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313 Arg Leu Ile Asn Ser Ala Asn Gly Val Ser Ser Lys Pro Leu Gln Asn
314           355           360           365
317 Gly Arg His Glu Asn Ile Glu Asn Gly Asn Val Pro Val Glu Asn Pro
318       370           375           380
321 Glu Asp Pro Gln Gln Asn Gln Glu Gln Gln Pro Pro Pro Gln Pro Pro
322 385           390           395           400
325 Pro Pro Glu Pro Glu Pro Val Glu Ala Asp Phe Leu Ser Pro Phe Ser
326           405           410           415
329 Val Pro Glu Ala Arg Gly Asp Lys Val Lys Trp Val Phe Thr Trp Pro
330       420           425           430
337 Leu Ile Phe Leu Leu Cys Val Thr Ile Pro Asn Cys Ser Lys Pro Arg
338       435           440           445
341 Trp Glu Lys Phe Phe Met Val Thr Phe Ile Thr Ala Thr Leu Trp Ile
342       450           455           460
345 Ala Val Phe Ser Tyr Ile Met Val Trp Leu Val Thr Ile Ile Gly Tyr
346 465           470           475           480
349 Thr Leu Gly Ile Pro Asp Val Ile Met Gly Ile Thr Phe Leu Ala Ala
350           485           490           495
353 Gly Thr Ser Val Pro Asp Cys Met Ala Ser Leu Ile Val Ala Arg Gln
354       500           505           510
357 Gly Leu Gly Asp Met Ala Val Ser Asn Thr Ile Gly Ser Asn Val Phe
358       515           520           525
361 Asp Ile Leu Val Gly Leu Gly Val Pro Trp Gly Leu Gln Thr Met Val
362       530           535           540
365 Val Asn Tyr Gly Ser Thr Val Lys Ile Asn Ser Arg Gly Leu Val Tyr
366 545           550           555           560
369 Ser Val Val Leu Leu Gly Ser Val Ala Leu Thr Val Leu Gly Ile
370           565           570           575
373 His Leu Asn Lys Trp Arg Leu Asp Arg Lys Leu Gly Val Tyr Val Leu
374           580           585           590
377 Val Leu Tyr Ala Ile Phe Leu Cys Phe Ser Ile Met Ile Glu Phe Asn
378       595           600           605
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389 <210> SEQ ID NO: 3

390 <211> LENGTH: 1845

391 <212> TYPE: DNA

392 <213> ORGANISM: Homo sapiens

394 <220> FEATURE:

395 <221> NAME/KEY: CDS

396 <222> LOCATION: (14)..(1825)

397 <223> OTHER INFORMATION:

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401 caggaattcc acc atg gcg ctc cgc ggg acc ctc cgg ccg ctc aaa gtt      49
402           Met Ala Leu Arg Gly Thr Leu Arg Pro Leu Lys Val
403           1           5           10
405 cgc agg agg cga gag atg ctg ccg cag caa gtc ggc ttc gtg tgc gcg      97
406 Arg Arg Arg Arg Glu Met Leu Pro Gln Gln Val Gly Phe Val Cys Ala
407           15           20           25

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VERIFICATION SUMMARY

DATE: 09/13/2004

PATENT APPLICATION: US/10/506,624

TIME: 16:13:22

Input Set : A:\pto.kd.txt

Output Set: N:\CRF4\09132004\J506624.raw

L:9 M:270 C: Current Application Number differs, Replaced Current Application No

L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:32 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:27

L:400 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:3,Line#:397



PCT

RAW SEQUENCE LISTING

DATE: 09/10/2004

PATENT APPLICATION: US/10/506,624

TIME: 16:22:29

Input Set : A:\PTO.FG.txt

Output Set: N:\CRF4\09102004\J506624.raw

3 <110> APPLICANT: Yamanouchi Pharmaceutical Co., Ltd.
5 <120> TITLE OF INVENTION: Novel potassium-dependent sodium/calcium exchanger
7 <130> FILE REFERENCE: Y0335PCT-693
C--> 9 <140> CURRENT APPLICATION NUMBER: US/10/506,624
C--> 9 <141> CURRENT FILING DATE: 2004-09-03
9 <150> PRIOR APPLICATION NUMBER: JP 2002-225114
10 <151> PRIOR FILING DATE: 2002-08-01
12 <150> PRIOR APPLICATION NUMBER: JP 2003-182989
13 <151> PRIOR FILING DATE: 2003-06-26
15 <160> NUMBER OF SEQ ID NOS: 8
17 <170> SOFTWARE: PatentIn version 3.1

Does Not Comply
Corrected Diskette Needed

(pg 1-2)

ERRORED SEQUENCES

786 <210> SEQ ID NO: 8
787 <211> LENGTH: 24
788 <212> TYPE: DNA
789 <213> ORGANISM: Artificial Sequence
791 <220> FEATURE:
792 <223> OTHER INFORMATION: Description of artificial Sequence: an artificially
synthesized
793 primer sequence
795 <400> SEQUENCE: 8
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E--> 797 1/17

delete

VERIFICATION SUMMARY

DATE: 09/10/2004

PATENT APPLICATION: US/10/506,624

TIME: 16:22:31

Input Set : A:\PTO.FG.txt

Output Set: N:\CRF4\09102004\J506624.raw

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L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:32 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:27
L:400 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:3,Line#:397
L:797 M:254 E: No. of Bases conflict, LENGTH:Input:17 Counted:25 SEQ:8
L:797 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:2
L:797 M:252 E: No. of Seq. differs, <211> LENGTH:Input:24 Found:25 SEQ:8